

Figure 1.

1 ILKQSERRRRSWSYRPWNTTENEGSQHRRSICSLGARSQSASINGWTEGNYNYIIEDED kv10.1.PRC
 1 HT-----KHGSRSTSSLPF----- hkv2.1.PRC
 1 HAE-----KAPPGLNRKTSRSTLSLPF----- hkv2.2.PRC

61 GEERDQWKDOLAEEDQOAGEVTTAKPEGPSDPPALLSTLNHVHGGHSYQLDYCELAGFEEK kv10.1.PRC
 15 -----EPMEIVRSKACSR-----VRLHVGGLAHEVCLWRTLDRLPR hkv2.1.PRC
 23 -----EPVDIIRSKTCSR-----VKIHVGGLNHEVCLWRTLDRLPR hkv2.2.PRC

121 TRLGRLATSTSRSRQLSLCDDYEEQTD EYFFDRDPAVFQLVYNEZLSGVLLVLDGLCPRR kv10.1.PRC
 51 TRLGKLRDCNTHDSLLEVCDDYSLD DNEYFFDRHPGAFSTILNPFYETGR LHHHEEHCALS hkv2.1.PRC
 59 TRLGKLRDCNTHESLLEVCDDVNLNE EYFFDRHPGAFSTILNPFYRTGK LHHHEEHCALS hkv2.2.PRC

181 FLRELGVWGVRLKYZTPRCCRICFERRDELSERLKIQHELRAQAQVEEAEELFRDMRFY G kv10.1.PRC
 111 FSQELDYWGIDEIYLESCCQARYHQKKEQHNEELRREAETLPEREGEE-----S-DNTCCA hkv2.1.PRC
 119 FGQELDYWGIDEIYLESCCQARYHQKKEQHNEELRREAETMRDGE GEE-----S-DNTCCP hkv2.2.PRC

241 PQRRLWNLMEKPFSSVAAKAIGVASSTFVLVSVVALALNTVEEMEQHSGQGE GGPDLRP kv10.1.PRC
 166 EKRKKLWDLLEKPNSSVAAKILAIISIMFIVLSTIALSLNTLPELOSLDEFGQSTDN--P hkv2.1.PRC
 174 DKRKKLWDLLEKPNSSVAAKILAIIVSILFIVLSTIALSLNTLPELOETDEFGQLNDN--R hkv2.2.PRC

301 ILEHVEMLCHGFFTLEYLLRLASTPDLRRFARSALNLVDLVAILFLYLQLLLECF TGE G H kv10.1.PRC
 224 QLAHVEAVCIAWFTMEYLLRFLSSPKKWKFFKGPLNAIDLLAILPYVVTIFLT----- hkv2.1.PRC
 232 QLAHVEAVCIAWFTMEYLLRFLSSPNKWKFFKGPLNVIDLLAILPYVVTIFLT----- hkv2.2.PRC

361 QRCQTVGSVGVKVGQVLRVMLHRIRPRIKLKLARHSTGLRAFUGFTLPCQVQQVGCCLLFLFIAH kv10.1.PRC
 277 ESNKSVLQFQNVRRVQVIFRIHRLIRKLKLARHSTGLQSLGFTLRRSYNELGLLILFLAH hkv2.1.PRC
 285 ESNKSVLQFQNVRRVQVIFRIHRLIRKLKLARHSTGLQSLGFTLRRSYNELGLLILFLAH hkv2.2.PRC

421 GIFTFSAAVYSVEHDPVSTNFTTIPHSWHA AVSISTVGYGDMYFETHLGRFFAFLCIAF kv10.1.PRC
 337 GIHIFSSLVFFAEKDEDDTKFKSIPASFWATITHTTVGYGDIYPKTLLGKIVGGLCCIA hkv2.1.PRC
 345 GINIFSSLVFFAEKDEDDTKFKSIPASFWATITHTTVGYGDIYPKTLLGKIVGGLCCIA hkv2.2.PRC

481 GIILNGMPSISILYJKFSDYYSKLKAYEYTTIRRE-----RGEVNFHQ--RARKKIAEC kv10.1.PRC
 397 GVLVIALPIPIIVNNFSEFYKEQKROEKAKRREALERAKRNGSIVSHHMDAFARSHIEM hkv2.1.PRC
 405 GVLVIALPIPIIVNNFSEFYKEQKROEKAKRREALERAKRNGSIVSHHMDAFARSHIEL hkv2.2.PRC

532 LL-----GSMNPQLTPR-QEN. kv10.1.PRC
 457 HDIVVEKNNGENMGKRDKVQDNHLSFNKWKHTKRTLSETSSSKSFETKEQGSPEKARS-- hkv2.1.PRC
 465 IDVAVERA GESA NTKDSADDNHLSFSRWWKWAR KALSETSSNKSFENKYQEV SQKDSHEQL hkv2.2.PRC

546 kv10.1.PRC
 514 -----SSSPQHNLNVQQL EDMYNKMAKTQ--SQPILNTRKESAAQSKP-KEELEHESIPSPVA hkv2.1.PRC
 525 NNTFSSSPQHLSAQKLEHLYNEITKTQPHSHBNPDCQEKPERPSAYEBEEIENEDEVVC PQE hkv2.2.PRC

546 kv10.1.PRC
 567 PLP-TRTEGVIDHRSMS SIDSFI SCATDFPEATRFSHSPLTSLPSKTGGSTAPEVGWRGA hkv2.1.PRC
 585 QLA VAQTEVIVDHKSTSSIDSFTSCATDFTEETER-----SPLP PPSASHLQM----- hkv2.2.PRC

546 kv10.1.PRC
 626 LGASGGRFVEANPSPDASQHSSFFIESPKSSMKTNNPLKLRALKVNFHEGDPSP LPLPVLG hkv2.1.PRC
 632 -----KFP TDLPGTEEHQRAR--GPPFLTLSREKGPAA RDGTLEYAPVDITVNL D AS G hkv2.2.PRC

546 kv10.1.PRC
 686 H--YHDFLRNRGSAAA AVAGLECATLLDKAVLSPESSIYTTASAKTPPRSPEKHTAIAF hkv2.1.PRC
 683 SQCG LHSPL OSDNATDSPKSSLKGSNPLKSRSLKVNFKENRGSA PQTPPSTARPLPVTTA hkv2.2.PRC

546 kv10.1.PRC
 743 NFEAGVHQYI OADTDDEGQLLYSVDS SPKSLPGSTSPKFSTGT RSEKNHFESSPLPTS P hkv2.1.PRC
 743 DFLSTTPQHIST-----ILL-----EETPSQGD RPCWALR PQLV RDL-----PKGCP P hkv2.2.PRC

546 kv10.1.PRC
 803 KFLRQNCIYS TEALTGKGPSGQEKCKLENHISP DVRVLP GGGAHGSTRDQSI hkv2.1.PRC
 787 GFP SRNCSLS-----LQERGCASLK hkv2.2.PRC

Figure 2.

↓ ↓

472	F	F	A	F	L	C	I	A	F	G	I	I	L	N	G	M	P	I	S	I	L	Y	N	K	F	S	Kv10.1
439	V	V	A	L	S	S	I	L	S	G	I	L	L	M	A	F	P	V	T	S	I	F	H	T	F	S	Kv6.1
388	I	V	G	G	L	C	I	A	G	V	L	V	I	A	L	P	I	P	I	I	V	N	N	F	S	Kv2.1	

Figure 3

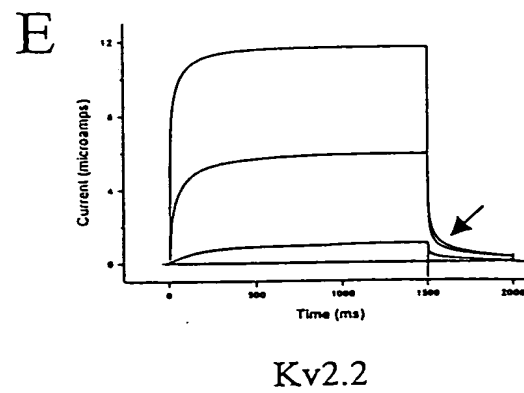
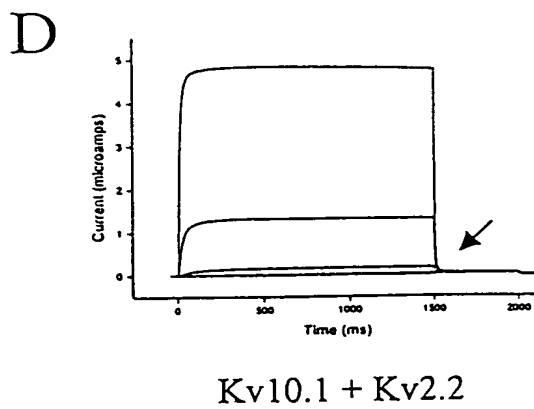
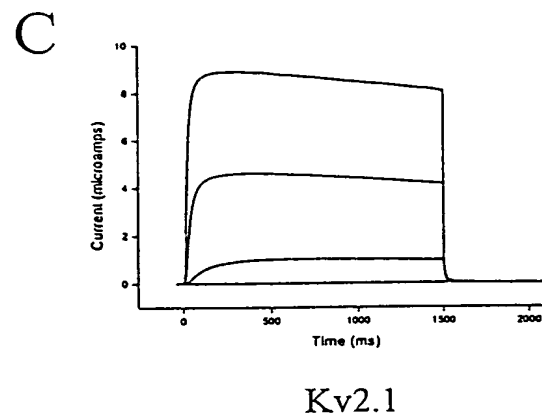
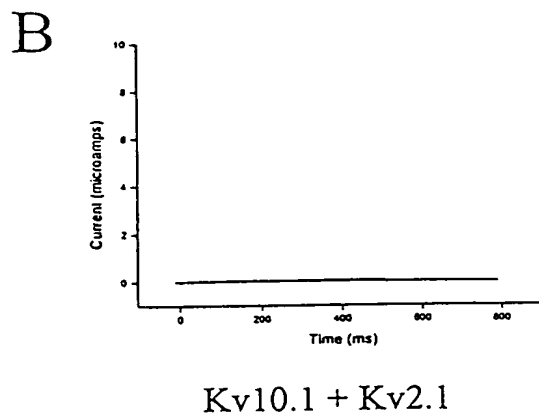
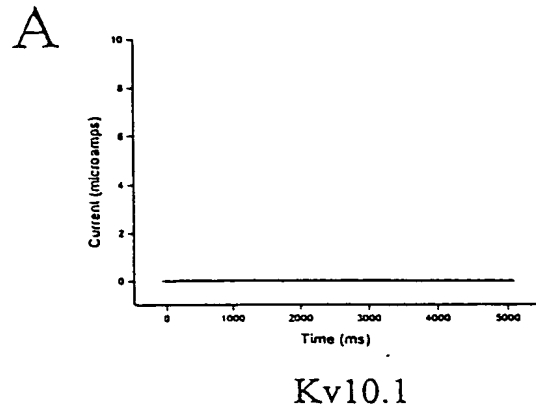
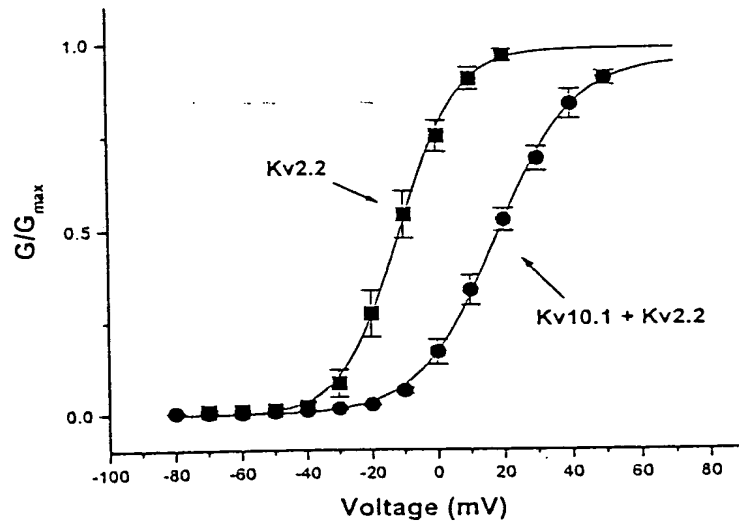
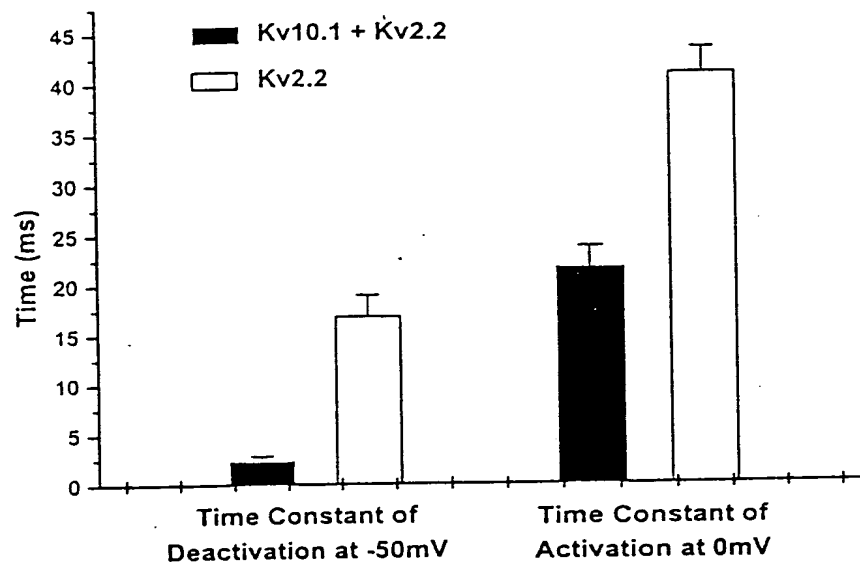


Figure 4

A.



B.



Kv10.1 mRNA

TR= Trace levels

- | | |
|-----|------------------|
| TR | Whole Brain |
| • | Fetal Brain |
| • | Trigeminal |
| • | DRG |
| TR | Frontal cortex |
| • | Hippocampus |
| + | Spinal cord |
| + | Substantia Nigra |
| • | Hypothalamus |
| • | Cerebellum |
| • | Kidney |
| • | Heart |
| +++ | Testis |
| • | Spleen |
| • | Pancreas |
| • | Bladder |
| + | Prostate |
| • | Liver |
| • | Skeletal Muscle |
| • | Placenta |
| • | Colon |
| + | Retina |

Figure 5